

# SEQUENCE LISTING

<110> Mack, David  
Gish, Kurt  
Wilson, Keith

<120> NOVEL METHODS OF DIAGNOSING CANCER, COMPOSITIONS, AND METHODS OF  
SCREENING FOR CANCER MODULATORS

<130> A-69192-1/DJB/JJD/AMS

<150> US 09/608,821

<151> 2000-06-30

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<170> PatentIn version 3.0

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gtc ttg aat tcc att ggt tca gat atc gac aat gta act cag cgt ctt Val Leu Asn Ser Ile Gly Ser Asp Ile Asp Asn Val Thr Gln Arg Leu 375 380 385 390	1207
cct att cag gat ata ctc tca gca ttc tct gtt tat gtt aat aac act Pro Ile Gln Asp Ile Leu Ser Ala Phe Ser Val Tyr Val Asn Asn Thr 395 400 405	1255
gaa agt tac atc cac aga aat tta cct aca ttg gaa gag tat gat tca Glu Ser Tyr Ile His Arg Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser 410 415 420	1303
tac tgg tgg ctg ggt ggc ctg gtc atc tgc tct ctg ctg acc ctc atc Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys Ser Leu Leu Thr Leu Ile 425 430 435	1351
gtg att ttt tac tac ctg ggc tta ctg tgt ggc gtg tgc ggc tat gac Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp 440 445 450	1399
agg cat gcc acc cgc acc acc cga ggc tgt gtc tcc aac acc gga ggc Arg His Ala Thr Pro Thr Thr Arg Gly Cys Val Ser Asn Thr Gly Gly 455 460 465 470	1447
gtc ttc ctc atg gtt gga gtt gga tta agt ttc ctc ttt tgc tgg ata Val Phe Leu Met Val Gly Val Gly Leu Ser Phe Leu Phe Cys Trp Ile 475 480 485	1495
ttg atg atc att gtg gtt ctt acc ttt gtc ttt ggt gca aat gtg gaa Leu Met Ile Ile Val Val Leu Thr Phe Val Phe Gly Ala Asn Val Glu 490 495 500	1543
aaa ctg atc tgt gaa cct tac acg agc aag gaa tta ttc cgg gtt ttg Lys Leu Ile Cys Glu Pro Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu 505 510 515	1591
gat aca ccc tac tta cta aat gaa gac tgg gaa tac tat ctc tct ggg Asp Thr Pro Tyr Leu Leu Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly 520 525 530	1639
aag cta ttt aat aaa tca aaa atg aag ctc act ttt gaa caa gtt tac Lys Leu Phe Asn Lys Ser Lys Met Lys Leu Thr Phe Glu Gln Val Tyr 535 540 545 550	1687
agt gac tgc aaa aaa aat aga ggc act tac ggc act ctt cac ctg cag Ser Asp Cys Lys Lys Asn Arg Gly Thr Tyr Gly Thr Leu His Leu Gln 555 560 565	1735
aac agc ttc aat atc agt gaa cat ctc aac att aat gag cat act gga	1783

Asn Ser Phe Asn Ile Ser Glu His Leu Asn Ile Asn Glu His Thr Gly	
570 575 580	
agc ata agc agt gaa ttg gaa agt ctg aag gta aat ctt aat atc ttt	1831
Ser Ile Ser Ser Glu Leu Glu Ser Leu Lys Val Asn Leu Asn Ile Phe	
585 590 595	
ctg ttg ggt gca gca gga aga aaa aac ctt cag gat ttt gct gct tgt	1879
Leu Leu Gly Ala Ala Gly Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys	
600 605 610	
gga ata gac aga atg aat tat gac agc tac ttg gct cag act ggt aaa	1927
Gly Ile Asp Arg Met Asn Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys	
615 620 625 630	
tcc ccc gca gga gtg aat ctt tta tca ttt gca tat gat cta gaa gca	1975
Ser Pro Ala Gly Val Asn Leu Leu Ser Phe Ala Tyr Asp Leu Glu Ala	
635 640 645	
aaa gca aac agt ttg ccc cca gga aat ttg agg aac tcc ctg aaa aga	2023
Lys Ala Asn Ser Leu Pro Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg	
650 655 660	
gat gca caa act att aaa aca att cac cag caa cga gtc ctt cct ata	2071
Asp Ala Gln Thr Ile Lys Thr Ile His Gln Gln Arg Val Leu Pro Ile	
665 670 675	
gaa caa tca ctg agc act cta tac caa agc gtc aag ata ctt caa cgc	2119
Glu Gln Ser Leu Ser Thr Tyr Gln Ser Val Lys Ile Leu Gln Arg	
680 685 690	
aca ggg aat gga ttg ttg gag aga gta act agg att cta gct tct ctg	2167
Thr Gly Asn Gly Leu Leu Glu Arg Val Thr Arg Ile Leu Ala Ser Leu	
695 700 705 710	
gat ttt gct cag aac ttc atc aca aac aat act tcc tct gtt att att	2215
Asp Phe Ala Gln Asn Phe Ile Thr Asn Asn Thr Ser Ser Val Ile Ile	
715 720 725	
gag gaa act aag aag tat ggg aga aca ata gga tat ttt gaa cat	2263
Glu Glu Thr Lys Lys Tyr Gly Arg Thr Ile Ile Gly Tyr Phe Glu His	
730 735 740	
tat ctg cag tgg atc gag ttc tct atc agt gag aaa gtg gca tcg tgc	2311
Tyr Leu Gln Trp Ile Glu Phe Ser Ile Ser Glu Lys Val Ala Ser Cys	
745 750 755	
aaa cct gtg gcc acc gct cta gat act gct gtt gat gtc ttt ctg tgt	2359
Lys Pro Val Ala Thr Ala Leu Asp Thr Ala Val Asp Val Phe Leu Cys	
760 765 770	
agc tac att atc gac ccc ttg aat ttg ttt tgg ttt ggc ata gga aaa	2407
Ser Tyr Ile Ile Asp Pro Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys	
775 780 785 790	
gct act gta ttt tta ctt ccg gct cta att ttt gcg gta aaa ctg gct	2455
Ala Thr Val Phe Leu Leu Pro Ala Leu Ile Phe Ala Val Lys Leu Ala	
795 800 805	
aag tac tat cgt cga atg gat tcg gag gac gtg tac gat gat gtt gaa	2503
Lys Tyr Tyr Arg Arg Met Asp Ser Glu Asp Val Tyr Asp Asp Val Glu	

810	815	820	
act ata ccc atg aaa aat atg gaa aat ggt aat aat ggt tat cat aaa			2551
Thr Ile Pro Met Lys Asn Met Glu Asn Gly Asn Asn Gly Tyr His Lys			
825	830	835	
gat cat gta tat ggt att cac aat cct gtt atg aca agc coa tca caa			2599
Asp His Val Tyr Gly Ile His Asn Pro Val Met Thr Ser Pro Ser Gln			
840	845	850	
cat tga tagctgatgt tgaactgct tgagcatcag gataactcaa gtggaaagga			2655
His			
855			
tcacagattt ttggtagttt ctgggtctac aaggactttc caaatccagg agcaacgcca			2715
gtggcaacgt agtgactcag gcgggcacca aggcaacggc accattggte tctgggtagt			2775
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ccctcccttc ctgtctattt ttgtttttta cttttttaca ctgagtttct atttagacac			2895
tacaacatat ggggtgtttt ttcccatggt atgcatttct atcaaaactc tatcaaatgt			2955
gatggctaga ttctaacata ttcccatgtg tggagtgtgc tgaacacaca ccagtttaca			3015
ggaaagatgc attttgtgta cagtaaacgg tgtatatacc ttttgttacc acagagtttt			3075
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atctgtcatt atcaaaaagt atcagcaatg aagaactggt cggacaaaat ttaacgttga			3675
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ctgattcatt tgaataaaaa ggaacttg			3764

<210> 4  
 <211> 855  
 <212> PRT  
 <213> Homo sapiens

<400> 4

Met Ala Leu Val Leu Gly Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn

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 Ser Phe Ser Gly Gly Gln Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp  
                     20                      25                      30  
 Asn Tyr Glu Leu Pro Ala Thr Asn Tyr Glu Thr Gln Asp Ser His Lys  
                     35                      40                      45  
 Ala Gly Pro Ile Gly Ile Leu Phe Glu Leu Val His Ile Phe Leu Tyr  
                     50                      55                      60  
 Val Val Gln Pro Arg Asp Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu  
                     65                      70                      75                      80  
 Gln Lys Ala Tyr Glu Ser Lys Ile Asp Tyr Asp Ile Val Tyr Tyr Glu  
                     85                      90                      95  
 Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu Phe Ile Ile Leu  
                     100                      105                      110  
 Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg Cys Cys Asn Lys  
                     115                      120                      125  
 Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn Gly Pro Phe Leu  
                     130                      135                      140  
 Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys Ile Ile Ile Ser  
                     145                      150                      155                      160  
 Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln Val Arg Thr Arg  
                     165                      170                      175  
 Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe Lys Asp Leu Arg  
                     180                      185                      190  
 Thr Leu Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr Ile Leu Ala Gln  
                     195                      200                      205  
 Tyr Asn Thr Thr Lys Asp Lys Ala Phe Thr Asp Leu Asn Ser Ile Asn  
                     210                      215                      220  
 Ser Val Leu Gly Gly Gly Ile Leu Asp Arg Leu Arg Pro Asn Ile Ile  
                     225                      230                      235                      240  
 Pro Val Leu Asp Glu Ile Lys Ser Met Ala Thr Ala Ile Lys Glu Thr  
                     245                      250                      255

Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys Ser Leu His Gln  
260 265 270

Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val Lys Thr Ser Leu  
275 280 285

Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His Pro Ser Ser Glu  
290 295 300

Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu Asn Ser Asn Pro  
305 310 315 320

Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu Asp Asn Val Asn  
325 330 335

Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln Gln Gly Tyr Gln  
340 345 350

Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln Thr Thr Thr Val  
355 360 365

Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly Ser Asp Ile Asp  
370 375 380

Asn Val Thr Gln Arg Leu Pro Ile Gln Asp Ile Leu Ser Ala Phe Ser  
385 390 395 400

Val Tyr Val Asn Asn Thr Glu Ser Tyr Ile His Arg Asn Leu Pro Thr  
405 410 415

Leu Glu Glu Tyr Asp Ser Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys  
420 425 430

Ser Leu Leu Thr Leu Ile Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys  
435 440 445

Gly Val Cys Gly Tyr Asp Arg His Ala Thr Pro Thr Thr Arg Gly Cys  
450 455 460

Val Ser Asn Thr Gly Gly Val Phe Leu Met Val Gly Val Gly Leu Ser  
465 470 475 480

Phe Leu Phe Cys Trp Ile Leu Met Ile Ile Val Val Leu Thr Phe Val  
485 490 495

Phe Gly Ala Asn Val Glu Lys Leu Ile Cys Glu Pro Tyr Thr Ser Lys  
500 505 510

Glu Leu Phe Arg Val Leu Asp Thr Pro Tyr Leu Leu Asn Glu Asp Trp  
515 520 525

Glu Tyr Tyr Leu Ser Gly Lys Leu Phe Asn Lys Ser Lys Met Lys Leu  
530 535 540

Thr Phe Glu Gln Val Tyr Ser Asp Cys Lys Lys Asn Arg Gly Thr Tyr  
545 550 555 560

Gly Thr Leu His Leu Gln Asn Ser Phe Asn Ile Ser Glu His Leu Asn  
565 570 575

Ile Asn Glu His Thr Gly Ser Ile Ser Ser Glu Leu Glu Ser Leu Lys  
580 585 590

Val Asn Leu Asn Ile Phe Leu Leu Gly Ala Ala Gly Arg Lys Asn Leu  
595 600 605

Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn Tyr Asp Ser Tyr  
610 615 620

Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn Leu Leu Ser Phe  
625 630 635 640

Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro Pro Gly Asn Leu  
645 650 655

Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys Thr Ile His Gln  
660 665 670

Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr Leu Tyr Gln Ser  
675 680 685

Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu Glu Arg Val Thr  
690 695 700

Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe Ile Thr Asn Asn  
705 710 715 720

Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr Gly Arg Thr Ile  
725 730 735



Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu Phe Ser Ile Ser  
740 745 750

Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala Leu Asp Thr Ala  
755 760 765

Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro Leu Asn Leu Phe  
770 775 780

Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu Pro Ala Leu Ile  
785 790 795 800

Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met Asp Ser Glu Asp  
805 810 815

Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn Met Glu Asn Gly  
820 825 830

Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile His Asn Pro Val  
835 840 845

Met Thr Ser Pro Ser Gln His  
850 855

<210> 5

<211> 5

<212> PRT

<213> Artificial

<220>

<223> Extracellular cytokine receptor motif found in many species.

<220>

<221> UNSURE

<222> (3)..(3)

<223> "Xaa" at position 3 can be any amino acid.

<400> 5

Trp Ser Xaa Trp Ser  
1 5